AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 6, line 32 to page 7, line 12, with the following paragraph:

Once the model of the protein has been obtained, the electrical potential function is calculated for the protein structure using standard methods in the art. There are a number of programs available for carrying out such calculations. These programs generally utilize a Poisson-Boltzmann (*Yang et al. 1993; Bashford et al. 1991; Warwicker et al. 1982; Antosiewicz et al. 1996*) procedure and solve the equations with a finite difference method or a finite element method. Exemplary programs that calculate the electrical potential function for proteins include UHBD (*Madura et al. 1995*), DelPhi (Accelrys Software Inc.) ~~(http://www.accelrys.com/insight/DelPhi page.html)~~, APBS (Adaptive Poisson Boltzmann Solver, which uses a finite element method) (*Baker et al. 2001*) and WHATIF: a molecular modeling and drug design program (*Vriend 1990*).

Please replace the paragraph between lines 37 and 41 on page 47, with the following paragraph:

Thompson et al. (1994) "CLUSTAL W: Improving The Sensitivity Of Progressive Multiple Sequence Alignment Through Sequence Weighting, Position-Specific Gap Penalties And Weight Matrix Choice." *Nucleic Acids Res.*, **22(22),** 4673-4680~~,~~ ~~http://www.ebi.ac.uk/clustalw~~.